

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/612,468B  
Source: 1FW/6  
Date Processed by STIC: 1/10/07

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

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1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06



IFW16

## RAW SEQUENCE LISTING

DATE: 01/10/2007

PATENT APPLICATION: US/10/612,468B

TIME: 09:43:35

Input Set : A:\D6622SEQ.txt

Output Set: N:\CRF4\01102007\J612468B.raw

3 <110> APPLICANT: Zhang, Jingwu Z.  
 4 Ho, Walter Kowk Keung  
 5 Zhang, Dongqing  
 6 Sun, Wei  
 8 <120> TITLE OF INVENTION: T Cell Receptor CDR3 Sequence and Methods for  
 9 Detecting and Treating Rheumatoid Arthritis  
 11 <130> FILE REFERENCE: D6622  
 13 <140> CURRENT APPLICATION NUMBER: US 10/612,468B  
 14 <141> CURRENT FILING DATE: 2003-07-02  
 16 <150> NUMBER OF SEQ ID NOS: 168

## ERRORED SEQUENCES

*see pp 1-3*  
 Does Not Comply  
 Corrected Diskette Needed

416 <210> SEQ ID NO: 29  
 417 <211> LENGTH: 21  
 418 <212> TYPE: DNA  
 419 <213> ORGANISM: Artificial Sequence  
 421 <220> FEATURE:  
 422 <221> NAME/KEY: primer\_bind  
 423 <223> OTHER INFORMATION: reverse primer specific for TCR BV11 used in real-time  
 424 PCR analysis  
 426 <400> SEQUENCE: 29 atgtgagggc ctggcagact c 21

688 <210> SEQ ID NO: 50  
 689 <211> LENGTH: 23  
 E--> 690 ~~<220>~~ DNA *<212>*  
 691 <213> ORGANISM: Artificial Sequence  
 693 <220> FEATURE:  
 694 <221> NAME/KEY: primer\_bind  
 695 <223> OTHER INFORMATION: forward primer specific for TCR BV22 used in real-time  
 696 PCR analysis

698 <400> SEQUENCE: 50  
 699 cacagatggg acaggaagtg atc 23

727 <210> SEQ ID NO: 53  
 728 <211> LENGTH: 21  
 729 <212> TYPE: DNA  
 730 <213> ORGANISM: Artificial Sequence  
 732 <220> FEATURE: *<221>*

E--> 733 ~~<21>~~ primer\_bind  
 734 <223> OTHER INFORMATION: reverse primer specific for TCR BV23 used in real-  
 735 time PCR analysis

## RAW SEQUENCE LISTING

DATE: 01/10/2007

PATENT APPLICATION: US/10/612,468B

TIME: 09:43:35

Input Set : A:\D6622SEQ.txt

Output Set: N:\CRF4\01102007\J612468B.raw

737 <400> SEQUENCE: 53  
 738 cagctccaag gagctcatgt t 21  
 740 <210> SEQ ID NO: 54  
 741 <211> LENGTH: 24  
 742 <212> TYPE: DNA  
 743 <213> ORGANISM: Artificial Sequence  
 745 <220> FEATURE:  
 746 <221> NAME/KEY: primer\_bind  
 747 <223> OTHER INFORMATION: forward primer specific for TCR BV24 used in real-time  
 748 PCR analysis *Insert a hard return*  
 750 <400> SEQUENCE: 54 ccaagataacc aggttaccca gttt 24

1271 <210> SEQ ID NO: 93  
 1272 <211> LENGTH: 20  
 1273 <212> TYPE: PRT  
 1274 <213> ORGANISM: Homo sapiens  
 1276 <220> FEATURE:  
 1277 <221> NAME/KEY: Domain  
 1278 <223> OTHER INFORMATION: CDR3 amino acid sequence of BV16 clonotype derived  
 1279 from ST specimen of RA patient

1281 <400> SEQUENCE: 93  
 1282 Tyr Phe Cys Ala Ser Ser Gln Ala Asp Gly Thr His Tyr Glu Gln  
 1283 5 10 15  
 1284 Phe Phe Gly Pro Gly

E--> 1285 ~~20~~ 20 *misaligned amino acid number*  
 1287 <210> SEQ ID NO: 94  
 1288 <211> LENGTH: 60 } <2127

E--> 1289 ~~(12)~~ DNA  
 1290 <213> ORGANISM: Artificial Sequence  
 1292 <220> FEATURE:  
 1293 <221> NAME/KEY: CDS  
 1294 <223> OTHER INFORMATION: CDR3 nucleic acid sequence of BV16 clonotype derived  
 1295 from ST specimen of RA patients

1298 <400> SEQUENCE: 94  
 1299 tattttctgtg ccagcagcca agctgacggg acccattacg agcagtactt 50  
 1300 cgggccgggc 60  
 1968 <210> SEQ ID NO: 140  
 1969 <211> LENGTH: 57 } <2127

E--> 1970 ~~(21)~~ DNA  
 1971 <213> ORGANISM: Artificial Sequence  
 1973 <220> FEATURE:  
 1974 <221> NAME/KEY: CDS  
 1975 <223> OTHER INFORMATION: CDR3 nucleic acid sequence of BV14 clonotype derived  
 1976 from ST specimen of RA patients

1978 <400> SEQUENCE: 140  
 1979 tactttctgtg ccagcagttt atcttcgaca gggaggggagc agtacttcgg gccgggc 57  
 2371 <210> SEQ ID NO: 168

## RAW SEQUENCE LISTING

DATE: 01/10/2007

PATENT APPLICATION: US/10/612,468B

TIME: 09:43:35

Input Set : A:\D6622SEQ.txt

Output Set: N:\CRF4\01102007\J612468B.raw

2372 &lt;211&gt; LENGTH: 54

2373 &lt;212&gt; TYPE: DNA

2374 &lt;213&gt; ORGANISM: Artificial Sequence

2376 &lt;220&gt; FEATURE:

2377 &lt;221&gt; NAME/KEY: CDS

2378 &lt;223&gt; OTHER INFORMATION: CDR3 nucleic acid sequence of BV14 clonotype derived

2379 from ST specimen of RA patients

2381 &lt;400&gt; SEQUENCE: 168

2382 tacttctgtg ccagcagttc cctcgctact gctgaagctt tctttggaca aggc 54

E--&gt; 2383 ??

E--&gt; 2385 ??

E--&gt; 2387 ??

E--&gt; 2389 ??

*delete*

## VERIFICATION SUMMARY

DATE: 01/10/2007

PATENT APPLICATION: US/10/612,468B

TIME: 09:43:36

Input Set : A:\D6622SEQ.txt

Output Set: N:\CRF4\01102007\J612468B.raw

L:426 M:301 E: (44) No Sequence Data was Shown, SEQ ID:29  
L:426 M:252 E: No. of Seq. differs, <211> LENGTH:Input:21 Found:0 SEQ:29  
L:690 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:698 M:282 E: Numeric Field Identifier Missing, <212> is required.  
L:733 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:750 M:301 E: (44) No Sequence Data was Shown, SEQ ID:54  
L:750 M:252 E: No. of Seq. differs, <211> LENGTH:Input:24 Found:0 SEQ:54  
L:1285 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:93  
L:1289 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:1298 M:282 E: Numeric Field Identifier Missing, <212> is required.  
L:1970 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:1978 M:282 E: Numeric Field Identifier Missing, <212> is required.  
L:2383 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:2385 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:168  
L:2385 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:2387 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:168  
L:2387 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1  
L:2389 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:168  
L:2389 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1